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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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%; Scor %; Pred 5; M	R EMBL; U23484; AAC46769.1;  R InterPro; IPR000719; Euk_pkinase.  R InterPro; IPR000719; Euk_pkinase.  R InterPro; IPR001841; Znf_ring.  R InterPro; IPR001841; Znf_ring.  R InterPro; IPR001807; zf-UBP.  R InterPro; IPR001607; zf-UBP.  R Pfam; PF00069; pkinase; 2.  R Pfam; PF00097; zf-C3Hc4; 1.  R Pfam; PF00148; zf-UBP; 1.  R Pfam; PF00184; RING; 1.  R Pfam; PF00184; RING; 1.  R PAGSITE; SM00184; RING; 1.  R RROSITE; PS00518; ZF_RING_1; FALSE_NEG.  R PROSITE; PS00518; ZF_RING_2; 1.  R PROSITE; PS0089; ZF_RING_2; 1.  R PROSITE; PS0089; ZF_RING_2; 1.  Hypothetical protein; Zinc-finger.  ZN_FING 908 945  R PROSITE; PS0089; ZF_RING_2; POLY-SER.  DOMAIN 1224 1229  DOMAIN 1234 1239  DOMAIN 1234 1238  POLY-SER.  DOMAIN 1235 1238  POLY-YSE.	s SWISS-PROT entry is copyright. It is produced the Swiss Institute of Bioinformatics European Bioinformatics Institute. There is by non-profit institutions as long as ified and this statement is not removed. Utilities requires a license agreement (See htt) send an email to license@isb-sib.ch).	the EMBL/GenB YHL010C AND	ns. Nematoda; Chromadorea inae; Caenorhabditis.	reated) ast sequen ast annota protein E	PRT	A	
ore 105; Di ed. No. 1.8 Mismatches	DOM; 1 SE_NEG. r. r-YPPE. Y-SER. Y-SER. Y-LYS.	ht. It is Bioinforma itute. Th is as long of removed ement (See sib.ch).	/GenBank AND S.P. TYPE ZIN	romador habditi	ted) sequence update) annotation updat tein EEED8.9 in c	; 123	LIGNMENTS	RNF6_HUMAN 2294_HUMAN RAPS_MOUSE YUES_CAEEL MKR1_MACEU MKR1_MOUSE MKR1_HUMAN PEXA_HUMAN PEXA_HUMAN RN23_HOUSE RN23_HOUSA ICPO_HSYEB MKR3_HUMAN
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InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00064; FYVE; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
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Q09463;
                                                                                         MKR3_MOUSE STANDARD; PRT; 544 AA G60764; 01-MAR-2002 (Rel. 41, Created) 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation updat Makorin 3 (Zinc-finger protein 127). MKRN3 OR ZFP127 OR ZNF127.
                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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               Jong
                                                                                 Mus musculus (Mouse)
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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16-OCT-2001
                        PubMed=10196368;
                                  SEQUENCE FROM N.
                                                    NCBI_TaxID=10090;
                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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               M.T.C.,
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               Α.Η.,
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Rodentia;
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               Caldwell K.A.,
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ein C16C10.7 in chr
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Pred. No. 3.7e
6; Mismatches
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                                                                                      Bouchard M.L., Cote S.; "The Drosophila melanogaster developmental gene zinc-finger-motif protein.";
                                                                                                                                                                                                                                                                     006003;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00184; RING; 1.
SMART; SM00356; ZnF_C3H1; 3.
PROSITE; PS00518; ZF_RING_1;
PROSITE; PS50089; ZF_RING_2;
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InterPro; IPR001841; Znf_ring.
Pfam; PF000697; zf-C3HC4; 1.
Pfam; PF00642; zf-CCCH; 3.
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"Imprinting of
                                                                          Gene 125:205-209(1993)
                                                                                                                           TISSUE=Embryo;
MEDLINE=93216124; PubMed=8462875;
                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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 SIMILARITY:
                                                 FUNCTION: REGULATION OF GENE EXPUTATIVE ROLE AS TRANSCRIPTION
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59444 MW;
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DNA-binding; Nuclear protein.
126 167
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01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tetratricopeptide repeat protein 3 (TPR repeat
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between
          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - \,
                                                                                                                                                           Tsukahara F., Hattori M., Muraki T., Sakaki Y.; "Identification and cloning of a novel cDNA bel tetratricopeptide repeat gene family from Down
                                                                                                                                                                                                       TISSUE=Fetal brain; MEDLINE=97103476; P
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-OCT-1996 (Rel. 34, I
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                                                                                                                                               region 21q22.2.";
                                                                                                                                                                                                                                                                              tetratricopeptide repeat domain chromosome 21.";
                                                                                                                                                                                                                                                                                                     Nagase T., Nomura N., Ohki M.;
"Identification of a novel human gene containing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTC3 OR TPRD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00518; ZF_RING_1; FALSE_NEG PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0004919; gol.
                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001841;
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTC3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 CTICSDFFDHSRDVAAIHCGHTFHLQCLIQWFETAPSRTCPQCRIQV
                                                  BIOCHEM. 120:820-827(1996).

BIOCHEM. 120:820-827(1996).

ALTERNATIVE PRODUCTS: 3 ISOFORMS; TRPDI (SHOWN HERE),
AND TPRDIII; SEEMS TO BE PRODUCED BY ALTERNATIVE SPLIC

TISSUE SPECIFICITY: FOUND IN ALL TISSUES EXAMINED.

SIMILARITY: CONTAINS 4 TPR REPEATS.

SIMILARITY: CONTAINS 1 RING-TYPPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffed and this statement is not removed. Usage by and for commercial
 European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; м97204; AAA28582.1; -.
JC1495; JC1495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAICIEAYKPTDTIRILPCKHEFHKNCIDPWL--IEHRTCPMCKLDV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                3:9-16(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208
284 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; Zinc-finger; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                         PubMed=8947847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 (
31973 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 92; DB
Pred. No. 0.00
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLN/PRO/SER-RICH.
; ECEE2D5EEDBA1E2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RING-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                              from
                                                                                                                                                                                                                                                                                                                                       Ichikawa H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2025
                                                                                                                                                                          Sakaki Y.;
el cDNA belonging
                                                                                                                                                                                                                                                                                          the Down syndrome region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
0.00019;
There are no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 284;
                                                                                                                                                            syndrome-critical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
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                                                                                                                                                                                                                                                                                                                                    RESULT
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Best Local
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                       01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Makorin 4 (Zinc-finger protein 127-Xp) (ZNE127-Xp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00518; ZE_RING_1; FALS PROSITE; PS50089; ZF_RING_2; 1. Repeat; TPR repeat; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
         the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents to the content in the content is not removed.
                                                                              escapes X chromosome inactivation.";

Submitted (NOV-1995) to the EMBL/GenBank/DDBJ data

-i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGERS.

-i- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
                                                                                                                                                   SEQUENCE FROM N.A.
Hendrich B.D., Longstreet M.,
                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                    Makorin 4 (Zinc-ri
MKRN4 OR ZNF127L1.
                                                                                                                                                                                                                                                                                                Q13434;
                                                                                                                                                                                                                                                                                                                                                                      1955 SSCEICHEVF-KSKNVRVLKCGHKYHKGCFKQWLK--GQSACPACQ 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
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                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                          Willard H.F.;
                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                             MKR4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
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                                                                                                                              "An X-linked homologue of the autosomal imprinted
                                                                                                                                                                                                                                                                                                                                                                                             2 SLCTICSDFFDHSRDVAAIHCGHTFHLQCLIQWFETAPSRTCPQCR 47
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PF00097; zf-C3HC4; 1.
; SM00184; RING; 1.
; SM00028; TPR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D83077; BAA11769.1; -. D84294; BAA12301.1; -. D84295; BAA12302.1; -. D84296; BAA12303.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
17; Conserv
requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat;
231
236
236
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576
6577
1957
1957
11957
1172
11172
11172
1
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                                                                                                                                                                                                                                                                                                             STANDARD;
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298
572
609
1997
456
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11029
11185
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233
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POLY-SER.

POLY-LYS.

POLY-LYS.

ARG/LYS-RICH (BASIC).

ARG/LYS-RICH (BASIC).

ARG/LYS-RICH (BASIC).

MISSING (IN ISOFORM TPRDII).

MISSING (IN ISOFORM TPRDIII).

MISSING (IN ISOFORM TPRDIII).
                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 91.5; D
Pred. No. 0.00
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPR
                                                                                                                                                                                                   Craniata; Vo
Catarrhini;
                                                                                                                                                    Gustashaw K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alternative
                                                                                                                                                                                                                                                                                                             485
                                                                                                                                                                                                             Vertebrata; Euteleostomi;
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                                                                                                                                                                                                      Hominidae;
                                                                                           3J databases.
[NGER.
                                                                                                                                                     Nicholls R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 splicing
                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                              gene
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         ons on its in no way commercial
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Best Local
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InterPro; IPR001841; znf ring.
Pfam; PF00097; zf-C3HC4; 1.
Pfam; PF00642; zf-CCCH; 4.
SMART; SM00184; RING; 1.
SMART; SM00356; ZnF_C3H1; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YHBO_YEAST
P38748;
O1-FEB-1995
O1-FEB-1995
16-OCT-2001
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ZN_FING
ZN_FING
DOMAIN
ZN_FING
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dov Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mc Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaug Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                               Science 265:2077-2082(1994).
-I- SIMILARITY: TO C.ELEGANS EEED8.9 AND S.POMBE
-I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nhan M., Ritkin L., NI.
Vignati D., Wilcox L.,
                                                                                                                                                                                                        modified
                                                                                                                                                                                                                          use
                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyce
Saccharomycetales; Saccharomycetaceae; Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00356; ZnF_C3H1; 4.
PROSITE: PS00518; ZF_RING_1;
PROSITE; PS50089; ZF_RING_2;
                                                                                                              EMBL;
                                                                                                                                                         or send
                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=S288C / AB972;
MEDLINE=94378003; PubMed=8091229;
                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete nucleotide sequence of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LCTICSDFF------DHSRDVAAIHCGHTFHLQCLIQW-----FETAPSRTCPQCRI 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match
                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffed and this statement is not removed. Usage by and for commercial
                           S0001002; YHL010C.
rPro; IPR001841; Znf_ring.
rPro; IPR001607; zf-UBP.
                                                                                          ; U11582; CAB34905.1; S46825; S46825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VCGICMEVVYEKANPNEHRFGILS-NCNHTFCLKCIRKWRSAKEFESRIVKSCPQCRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U41315; AAA99070.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                         an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an email to license@isb-sib.ch).
                                                                                                                                                                           requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat.
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485 AA;
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31,
40,
kDa
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32.8%;
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Last annotation update)
protein in PRPS4-STE20
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C3H1-TYPE 2.
C3H1-TYPE 3.
MAKORIN-TYPE (
RING-TYPE 4.
C3H1-TYPE 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomycotina; Saccharomycetes; cetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3H1-TYPE 4.
AE28B962544CEFFE CRC64;
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No. 0.00047;
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                                                                                                                                                                                                                                                                                                                                                                                                                         cerevisiae chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouser L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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RESULT 8
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Best Local
                                                                                                                           PIR; S15788; S15788.

WormPep; ZK637.14; CE00432.
InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.

SMART; SM00184; RING; 1.

SMART; SM00184; RING; 1.

PROSITE; PS000518; ZF_RING_1; FALSE_NEG.
PROSITE; PS50089; ZF_RING_2; 1.

Hypothetical protein; Zinc-finger.
ZN_FING 72 134

RING-TYPE.
SEQUENCE 161 AA; 18847 MW; F5EF9F3A83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00097; zf-C3HC4; 1.
Pfam; PF02148; zf-UBP; 1.
SMART; SM00184; RING; 1.
SMART; SM00290; ZnF_UBP; 1.
SMART; SM00290; ZnF_UBP; 1.
PR0SITE; PS00518; ZF_RING_1; FALSE_NEG.
PROSITE; PS50089; ZF_RING_2; 1.
PROSITE; PS50089; ZF_RING_2; 1.
Hypothetical protein; Zinc-finger.
Lypothetical protein; Zinc-finger.
ZN_FING_240_280_RING_TYPE.
                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and the modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BRISTOL N2;
MEDLINE-92168156; PubMed-1538779;
Sulston J., Du Z., Thomas K., Wilson R., Hillier L.,
Sulston J., Du Ze., Thomas K., Wilson R., Hillier L.,
Halloran N., Green P., Thierry-Mieg J., Qiu L., Dear
Craxton M., Durbin R.K., Berks M., Metzstein M., Hawk
Ainscough R., Waterston R.;
                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical ZK637.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1993
16-OCT-2001
                                                                                                                                                                                                                                                                             EMBL; Z11115; CAA77447.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       "The C. elegans genome sequencing project: Nature 356:37-41(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P30631;
01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 LPTCPVCLERMDSETTGLVTIPCQHTFHCQCLNKW----KNSRCPVCR
                                                                   Local
72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LSLCTICSDFFD-HSRDVAAIHCGHTFHLQCLIQWFETAPSRTCPQCR 47
                           4
                                                                                  Match
CAICLDNLQNNVDIPEDHVIKEELKIDPTTFGTTVIVMPCKHRFHYFCLTLWLEA--QQT 129
                         CTICSDFFDHSRDVAAIH---
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                                                       Similarity 20; Conser
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(Rel.
(Rel.
18.8
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                                                         Conservative
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27, Last sequence update)
40, Last annotation update)
40 kDa protein ZK637.14 in chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67503 MW;
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                                                                      30.5%;
                                                    Score 89.5; D
Pred. No. 0.00
5; Mismatches
                                                       5.
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                                                                                                                               RING-TYPE.; F5EF9F3A83A9C027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.00056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161
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                                                      DB 1;
).00022;
hes 20;
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                        CGHTFHLQCLIQWFETAPSRT
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S., Cou
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RESULT 9
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ID RN12_MOUSE
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Best Local
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16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
RING finger protein
                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Opposing developmental functions of positive and coregulators of LIM homeodomain factors."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bach
                                                                                                            Transcription regulation; Zinc-finger.
DOMAIN 415 484 SER-RICH.
ZN_FING 546 587 RIG-TYPE
DOMAIN 447 461 POLY-SER.
SEQUENCE 600 AA; 66470 MW; E682995
                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99364422; PubMed=10431247;
Bach I., Rodriguez-Esteban C., Carriere
Rose D.W., Glass C.K., Andersen B., Izpi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RING finger LIM domain-binding protein) (R-LIM).
                                                                                                                                                                                                       Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                           EMBL; AF069992; AAD34209.1; -. MGD; MGI:1342291; Rnf12.
                                                                                                                                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                               InterPro; IPR001841; Znf_ring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130
 543
                         _
                                                                                                                                                                                                                                                                                                                                                                           THANSCRIFTION ELECTION COMPLEX.
DEACETYLASE COREPRESSOR COMPLEX.
SUBUNIT: ASSOCIATES WITH LIM/HOMEOBOX
SIMILARITY: CONTAINS 1 RING-TYPE ZINC
                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPQCRIQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CT-2001 (Rel. 40, Last sequence update)
CT-2001 (Rel. 40, Last annotation update)
finger protein 12 (LIM domain interacting
              LSLCTICSDFFDHSRDVAAIHCGHTFHLQCLIQWFETAPSRTCPQCR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CPTCRQKV 137
LKTCSVCITEYTEGDKLRKLPCSHEFHVHCIDRWL -- SENSTCPICR
                                                              Similarity
                                                                                                                                                                             PS00518; ZF_RING_1; FALSE_NEG PS50089; ZF_RING_2; 1.
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40,
                                                             30.4%;
29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                 10;
                                                Score 89; DB
Pred. No. 0.00
LO; Mismatches
                                                                                                          POLY-SER.
: E68299530126E41D
                                                                                                                                         RING-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           600
                                                                                                                                                                                                                                                                                                                                There are no
                                                              DB 1;
0.00089
                                                                                                                                                                                                                                                                                                                                                                                      FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homeodomain transcription acetylase complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bhushan A., Kr
Belmonte J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      databases
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                                                                        Length 600
                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              negative
                                                 Indels
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         finger protein)
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SIN3A/HISTONE
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RESULT

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LCTICSDFFDHSRDVAAIHCGHTFHLQCLIQWFETAPSRTCPQCRIQV

Matches

l Similarity 18; Conserv

Conservative

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Indels

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CBLC_HUMAN
IID CELC_HUMAN
AC 09ULVM
AC 09ULVM
AC 09ULVM
DI 16-OCT
RI SIGUIM
RA KIM M.
[1]
RA KIM M.
RA KIM M.
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CC -!- FU
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CC -!- SI
CC OI SEN
                  Query Match
Best Local
                                                                                                                                                                                                                                        Pfam; PF02262; Cbl_N; 1.
Pfam; PF02761; Cbl_N2; 1.
Pfam; PF02762; Cbl_N3; 1.
Pfam; PF00099; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
SMART; SM00252; SH2; 1.
PR0SITE; PS00518; ZF_RING_1; 1.
PR0SITE; PS05089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9ULV8; O9Y5Z3; O9Y5Z2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal transduction protein CBL-C CBLC OR CBL3.
                                                                                                           CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Pancreatic adenocarcinoma; MEDLINE=99289203; PubMed=10362357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 239:145-154(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kim M., Tezuka T., Suzuki Y., Sugano S., Hirai M., "Molecular cloning and characterization of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (LONG FORM). MEDLINE=20035821; PubMed=10571044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).

Mortazoa, Chordata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. Thuse by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003153; Cbl_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keane M.M., Ettenberg S.A., Nau M.M., Banerjee
                                                                                                                                                       VARSPLIC
                                                                                                                                                                            ZN_FING
                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                        Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000980; InterPro; IPR001841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; AB028645; BAA
; AF117646; AAD
; AF117647; AAD
; P22681; 1B47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                              protein; Zinc-finger; Phosphorylation; Alternative 89 92 NUCLEAR LOCALIZATION SIGNAL (F
                                                                                                        351
261
234
474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAA86298.1; -. AAD34341.1; -. AAD34342.1; -.
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                                                                                        92
390
306
234
52468
                  30.0%;
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                                                                                                             WW.
Score 88; DB
Pred. No. 0.00
9; Mismatches
                                                                                                           RING-TYPE.
MISSING (IN SHORT ISOFORM).
T -> N (IN REF. 2).
; 91013DDF12828242 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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(SH3-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein CBL-C) (CBL-3).
                                         Length, 474;
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RESULT 11
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A Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
A Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
A Wagatsuma M., Hosoiri T., Kaku Y., Koddira H., Kondo H., Sugawara M.,
A Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
A Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
A Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
A Ninomiya K., Imayanagi T.;
A Ninomiya K., Iwayanagi T.;
A Submitted (PEB-2000) to the EMBL/GenBank/DDBJ databases.
A Submitted (PEB-2000) to the EMBL/GenBank/DDBJ databases.
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Q9NVW2; Q9Y598;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
RING finger protein 12 (LIM domain interacting RING finger protein)
(RING finger LIM domain-binding protein) (R-LIM) (NY-REN-43 antigen
(RING finger LIM domain-binding protein) (R-LIM) (NY-REN-43 antigen)

(RING finger LIM domain-binding protein) (R-LIM) (NY-REN-43 antigen)
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MEDLINE-99438124; PubMed=10508479;
Scanlan M.J., Gordan J.D., Williamson
Jongeneal V., Gure A.O., Jager D., Jagold L.J.;
                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
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-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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PROSITE; PS50089; ZF_RING_2; 1.
Hypothetical protein; Transmembrane;
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InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
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01-MAR-1989
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J. Cell ":"
                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Torpedo californica (Pacífic electric ray).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chelasmobranchii, Squalaea; Hypnosqualaea; Pristiorajea; ETorpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
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EMBL; J02952; AAA49282.1; EMBL; J02953; AAA49283.1; PIR; A28009; A28009.
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Carr C., McCourt D., Cohen J.B.;
"The 43-kilodalton protein of Torpedo nicotinic postsynaptic membranes: purification and determination of primary structum
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16-OCT-2001 (Rel. 40, Last annotation update)
43 kDa receptor-associated protein of the synapse (
Acetylcholine receptor-associated 43 kDa protein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              postsynaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
                                                                                                                                                                                             ALTERNATIVE PRODUCTS: THERE ARE AT LEAST TWO DISTINCT EXPRESSED, WHICH DIFFER IN THEIR C-TERMINUS.

DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO PART OF REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE IMPORTAN INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER. SIMILARITY: BELONGS TO THE RAPSYN FAMILY.

SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                Cell Biol. 107:1113-1121(1988).

FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES, IT MAY LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON, POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.

SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC
                                                                                                                                                                                                                                                                                                                     MEMBRANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYCKERV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VCAVCGGRLDDSEHVHDADAVVTTKMVEDEDEKLYKLSCGHVFHEFCIRGWVVVGKLQTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCTICS---DFFDHSRDVAAI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 (Rel. 10, Creat
0 (Rel. 15, Last
1 (Rel. 40, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26:7090-7102(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Merlie J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    43K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411
                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein contains covalently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata; Chondrichthyes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --HCGHTFHLQCLIQWFETAPSRTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                    DISTINCT PROTEINS
                                                                                                                                                                                                                                                     IMPORTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RAPSYN)
) (43 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Merlie J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Batoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       electric organ
                                                                                                                                                                                                                                                                                                                                                                                    STABILIZING TES. IT MAY
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Best Local
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Pfam; PF00515; TPR; 5.
Pfam; PF0097; zf-C3HC4; 1.
PRINTS; PR00217; POSTSYNAPTIC.
ProDom; PD012428; Postsynaptic; 1
SMART; SM00184; RING; 1.
SMART; SM00028; TPR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00405; 43_KD_POSTSYNAPTIC; PS00518; ZF_RING_1; FALSE_NEG PROSITE; PS50089; ZF_RING_2; 1.
Synapse; Postsynaptic membrane; Cytos)
                                                                                                by provirus tagging.";
Cell 65:737-752(1991).
                                                                                                                              Gulden
                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=91249381; PubMed=1904008;
van Lohuilzen M., Verbbeek S., Scheijen B.,
                                                                                                                                                                                                        Haupt Y., Alexander W.S., Barri G., Klinken S.P., Adams J "Novel zinc finger gene implicated as myc collaborator by retrovirally accelerated lymphomagenesis in E mu-myc tran
                                                                                                                                                                                                                                                                                                                                     01-MAY-1992 (Rel.
01-MAY-1992 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIPID
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=91249382; PubMed=1904009;
                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                 Polycomb complex BMI1 OR BMI-1.
                                                                                                                                                                                                                                                                                                                                                                      p25916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myristate;
                                                                                                                    "Identification of cooperating
                                                                                                                                                                                                                                                                                                                                                                                   BMI1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                       362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR001237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CTICSDFF-DHSRDVAAIHCGHTFHLQCLIQWFETAPSRTCPQCR
SUBCÉLLULAR LOCATION: Nuclear.
TISSUE SPECTFICITY: DEFECTED IN MOST ORGANS
LEVELS IN THYMUS, HEART, BRAIN AND TESTIS.
DISEASE: COOPERATES WITH THE MYC ONCOGENE TO
                                                     FUNCTION: INVOLVED IN MAINTAINING T
STATE OF GENES. MODIFIES CHROMATIN,
IN 1TS EXPRESSIBILITY.
SUBUNIT: COMPONENT OF THE CHROMATIN
                                            (PCG)
                                                                                                                                                                                     65:753-761(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                       CGLCGESIGDQNSQLQALPCSHLFHLKCL----QTNGNRGCPNCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
16; Conserv
                                                                                                                              Berns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 AA;
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404
389
361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -tinger;
                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                       22,
40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 402
195
404
411
361
393
                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46321 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Postsynaptic
                                                                                                                                                                                                                                                                                                                                       Last sequence u
                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alternative splicing
                                                                                                                                                                                                                                                                                                                             BMI-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 87.5; I
Pred. No. 0.00
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (
MISSING (IN SHORT
Y -> T (IN REF. 2
N -> D (IN REF. 2
Y -> T (IN REF. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYRISTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FALSE_NEG
                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Sciurognathi; Muridae;
                                                      CHROMATIN-ASSOCIATED
                                                                                                                    oncogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4D26262679FC9B4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.5; DB 1;
No. 0.00095;
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on update)
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                                                                                                                                                                                                                                                                                                                                                                                324
                                                                                    THE
                                                                          RENDERING
                                                                                                                     j.
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                                                                          TRANSCRIPTIONALLY REPRESSIVE ENDERING IT HERITABLY CHANGED
                                                                                                                     H
                                                                                                                                        Wientjens
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                                                                                                                    mu-myc transgenic
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                     WITH
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                                                                                                                                                                                                                                                                                                                                                                                                                                       402
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                                                      POLYCOMB
                                                                                                                                                                                                                                                                                  Euteleostomi; Murinae; Mus
                                                                                                                                                                                                                             J.M.;
                      EXPRESSION
                                                     COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
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                                                                                                                     mice
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ТО

PRODUCE

B LYMPHOMAS

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RESULT AS
BMINI_H
BMINI_H
AC P35226
DT 01-FEB
OC Mammal
OX NCBI_T
RN [1]
RP SEQUEN
RC TISSUE
RX MALKema
RT Chara
RT Chara
RT Chara
RT Chara
RT Chara
RT SEQUEN
RC TISSUE
RX SUBmitt
CC -:-FU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 29.7%;
Best Local Similarity 33.3%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          BMI1_HUMAN STANDARE
P35226; Q96E37;
01-FEB-1994 (Rel. 28, C
01-FEB-1994 (Rel. 28, I
01-MAR-2002 (Rel. 41, I
Polycomb complex protei
                                                                                                   Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: INVOLVED IN MAINTAINING THE TRANSCRIPTIONALLY REPRESSIVE
STATE OF GENES. MODIFIES CHROMATIN, RENDERING IT HERITABLY CHANGED
IN ITS EXPRESSIBILITY.
                                                                                                                                                                                                                                                       TISSUE-Erythrocyte;
MEDLINE-94093545; PubMed-8268912;
Alkema M.J., Wiegand J., Raap A.K., Berns A., v
"Characterization and chromosomal localization"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M64067; AAA37299.1; -.
EMBL; M64068; AAA37301.1; ALT_SEQ.
EMBL; M64279; AAA37300.1; -.
PIR; A39523; A39523.
PIR; A39524; A39524.
MGD; MGI:88174; Bmil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                     TISSUE=Muscle;
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   oncogene BMI-1.";
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00518; ZF_RING_1; 1.

PROSITE; PS50089; ZF_RING_2; 1.

Chromatin regulator; Nuclear protein; Transcription regulation; Repressor; Zinc-finger; Proto-oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         w
                   SUBCELLULAR LOCATION: Nuclear.
DISEASE: COOPERATES WITH THE MYC
SIMILARITY: CONTAINS 1 RING-TYPE
                                                                                    SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LCTICSDFFDHSRDVAAIHCGHTFHLQCLIQWFETAPSRTCPQCRIQV 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                             complex protein
                                                                                                                                                                                                                                  Genet.
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81
249
324 AA;
                                                                                      COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                2:1597-1603(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 R
95 N
324 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                      OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                             BMI-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 87; DB
Pred. No. 0.00
L2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RING-TYPE.
NUCLEAR LOCALIZATION SIGNAL PRO/SER-RICH.
                                                                                   CHROMATIN-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AD7DECDB6B29DCE5 CRC64;
                     ONCOGENE TO
ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326
                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
0.00088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                            Hominidae;
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n of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 324
                                      PRODUCE
                                                                                                                                                                                                                                                              Lohuizen M.;
the human proto-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                 POLYCOMB
                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                    LYMPHOMAS
                                                                                    COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
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SO FITTERS
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Z147_MOUSE
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                         Orimo A., Inoue S., Ikeda K., Noji S., Muramatsu "Molecular cloning, Structure, and expression of responsive finger protein Efp. Co-localization wimana in target organs.";
J. Biol. Chem. 270:24406-24413(1995).
-!- FUNCTION: MEDIATES ESTROGEN ACTION IN VARIOUS-
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001841; Znf_ring.
Pram; pr00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
SMART; SM00184; RING; 1.
PROSITE; ps00518; zf_RING_1; 1.
PROSITE; ps005089; zf_RING_2; 1.
Chromatin regulator; Nuclear protein; Transcription regulation; Chromatin regulator; Proto-oncogene.
Repressor; Zinc-finger; Proto-oncogene.
Repressor; Zinc-finger; Proto-oncogene.
ZN_FING_21
STATEMENT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
CONFLICT
SEQUENCE
                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                  the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Uterus, Ovary, and Placente MEDLINE=96025835; PubMed=7592654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Zinc finger protein 147 (Estrogen responsive
ZNF147 OR ZFP147 OR EFP.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L13689; AAA19873.1; -. EMBL; BC011652; AAH11652.1; -. MIM; 164831; -.
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                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL
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                                                                  MGD; MGI:102749;
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16; Conserv
                   :102749; Zfp147.
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Pred. No. 0.00
12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR001841; Znf_ring.
pfam; pF00622; SpRy; 1.
pfam; pF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
SMART; SM00449; SPRY; 1.
PROSITE; PS00518; ZE_RING_1; 1
PROSITE; PS50089; ZE_RING_2; 1
Zinc_finger; Coiled Coil.
                                                                                                                                                                 between
the Euro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21481893; PubMed=11597136;
Gray T.A., Azama K., Whitmore K.,
"Phylogenetic conservation of the
zinc-finger protein, antisense to
genomics 77:119-126(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G., Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W., Tao J., Huang Q.-H., Zhou J., Hu G.-X., G. J., Chen S.-J., Chen Z.; "Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic stem/progenitor cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                         Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-- TISSUE SPECIFICITY: Widely expressed.
-- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=21481893;
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sapiens (Human).

chordata;
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AF302084; AAG30426.1; AF277170; AAG27595.1;
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                                                                    non-profit institutions as long as its content is d and this statement is not removed. Usage by and for s requires a license agreement (See http://www.isb-sib.an email to license@isb-sib.ch).
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514
634 AA;
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Pred. No. 0.0017;
6; Mismatches 1
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SPRY.
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makorin-2 gene,
the rafl proto-c
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Q9ERV1; Q9D0L9;
01-MAR-2002 (Rel
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01-MAR-2002 (Re
Rawai J., Shinagawa A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.
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ZN_FING
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CONFLICT
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SEQUENCE
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                                                                                                                                                                                      MEDLINE=21481893; pubMed=11597136; Gray T.A., Azama K., Whitmore K., "Phylogenetic conservation of the zinc-finger protein, antisense to Genomics 77:119-126(2001).
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SMART; SM00356; ZnF_C3H1; 4.
PROSITE; PS00518; ZF_RING_1;
PROSITE; PS50089; ZF_RING_2;
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InterPro; IPR001841;
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                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Embryo; MEDLINE=21085660; PubMed=11217851;
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                SEQUENCE FROM
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PF00097; zf-C3HC4; 1.
PF00642; zf-CCH; 4.
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BC001799;
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AF277166;
AF277167;
AF277168;
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C3H1-TYPE 3.
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RING-TYPE 4.
C3H1-TYPE 4.
F -> V (IN REF. 2 AN
K -> E (IN REF. 2).
W; 02B6B7A8BD382DDC C
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15-JUL-1998 (I
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SPAC16E8.13.
                                    This
                                                                                 Oliver K., Harris D., Barrell B.G., Rajandream M.A., Woo
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO YEAST YHLO10C AND C.ELEGANS EEED8.9.
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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InterPro; IPR001841; Znf_ring.
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Pfam; PF00642; zf-CCCH; 4.
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(Rel. 36,
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protein C16E8.13 in chromosome
                                 is copyright.
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C3H1-TYPE 2.
C3H1-TYPE 3.
MAKORIN-TYPE CYS-HIS.
RING-TYPE.
C3H1-TYPE 4.
C3H1-TYPE 4.
L -> F (IN REF. 2).
M; 5F268E6B9D9A6C9F CRC64;
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Pred. No. 0.0013;
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"mel-18, a Polycomb group-related mammalian gene, encodes a
transcriptional negative regulator with tumor suppressive ac
EMBO J. 14.5672-5678 (1995).

EMBO J.
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01-MAY-1992 (Rel. 22, Last sequence u
01-MAY-2002 (Rel. 41, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=91060627; PubMed=2246278;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Pfam; PF02148; zf-UBP; 1.
SMART; SM00184; RING; 1.
SMART; SM00290; ZnF_UBP; 1.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
PROSITE; PS0069; ZF_RING_2; 1.
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"Expression of novel_DNA-binding protein
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InterPro; IPR001607; zf-UBP.
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DISEASE: PROBABLY RELATED TO TUMORGENESIS
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ZN_FING
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"Cloning and chromosome mapping "Cloning and chromosome mapping with the control of the
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Transcription regulation; Repressor; Zinc-finger; DNA-binding;
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                                      + +
                                                                                                                                            Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: TRANSCRIPTIONAL REPRESSOR. BINDS SPECIFICALLY TO DNA SEQUENCE S'GACTMGAGT-3'. HAS A TUMOR SUPPRESSOR ACTIVITY MAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEUMAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND PLAY A ROLE OF 
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                                                                    CELL DEVELOPMENT.
SUBCELLULAR LOCATION: Nuclear
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MGI:99161; Zfp144
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    PF00097; zf-C3HC4; 1.
; SM00184; RING; 1.
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DETECTED
PLACENTA
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annotation update)
(Zinc finger protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
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PHOSPHORYLATION (BY CAPK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
C23031B8B9E30108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RING-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with
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IN ALL TISSUE EXAMINED LUNG AND KIDNEY AND LOV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human Mel-18 gene which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .0012;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 342;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Τ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
   LOW EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yoshida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    motif.";
                                         WITH HIGH
                                                                                                                                                                                  ACTIVITY
                                                                                                                                                NEURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 22
CBL_HUMAN
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            CBL_HUMAN P22681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nuclear
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  v-cbl was generated by a large truncation
domain and a leucine zipper-like motif.";
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                             Signal
                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00518; ZF_RING_1; 1. PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00097; zf-C3HC4; SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; JN0717; JN0717. MIM; 600346; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through
                                                                                 Nature 398:84-90(1999).
                                                                                                   Meng W., Sawasdikosol S., Burakoff S.J., "Structure of the amino-terminal domain objiding site on ZAP-70 kinase.";
                                                                                                                                        x-ray CRYSTALLOGRAPHY (2.2 ANGSTROMS) MEDLINE=99176421; PubMed=10078535;
                                                                                                                                                                                                                        Blake T.J.,
                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                           Oncogene
                                                                                                                                                                                                            "The sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001841;
                                                                                                                                                                                                                                   MEDLINE=91232862;
                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LCTICSDFFDHSRDVAAIHCGHTFHLQCLIQWFETAPSRTCPQCRIQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN LIVER, PANCREAS AND SKELETAL MUSCLE.
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
SURFACE.
SUBUNIT: ASSOCIATES WITH NCK VIA
SUBCELLULAR LOCATION: Nuclear.
PTM: PHOSPHORYLATED ON TYROSINE.
SIMILARITY: CONTAINS 1 RING-TYPE
                                                                                                                                                                                                                                                                                                                    OR CBL2.
                                                       FUNCTION: PARTICIPATES IN SIGNAL TRANSDUCTION IN HEMATOPOIETIC CELLS: ADAPTOR PROTEIN THAT FUNCTIONS AS A NEGATIVE REGULATOR MANY SIGNALLING PATHWAYS THAT START FROM RECEPTORS AT THE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCALCGGYFIDATTI - - VECLHSFCKTCIVRYLET - - NKYCPMCDVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC004858; AAH04858.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D13969; BAA03074.1; -.
                                                                                                                                                                                                                                                                                                                           transduction protein
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14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein.
                                                                                                                                                                        nd a leucine zipper-like 6:653-657(1991).
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344 AA;
                                                                                                                                                                                                        Shapiro M., Morse H.C. III, Lauveces of the human and mouse c-cbl
                                                                                                                                                                                                                                                                                                       (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                               N.A.
                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57
95
344
37788 1
                                                                                                                                                                                                                        PubMed=2030914;
ro M., Morse H.C.
                                                                                                                                                                                                                                                                                Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Znf_ring.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                               CBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 86;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.004; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEAR LOCALIZATION PRO/SER-RICH.; A910BCD4C0CE9927 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RING-TYPE
                                                                                                                                                                                                                                                                                 Catarrhini;
                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                              (Proto-oncogene
                                                                                                                                                                                                                        III, Langdon W.Y.;
                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zinc-finger;
  ZINC FINGER
                                    ITS
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                                                                                                                                                    QF.
                                                                                                                                                                                                                                                                                                                                        update)
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                                                                                                                  of Cbl complexed
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                                                                                                                                                                                                                                                                                                                                                                                       ΑA
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                                                                                                                                                                                                                                                                                 Hominidae;
                                                                                                                                                                                                             proto-oncogenes show
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                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 344
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                                                                                                                                                                                                                                                                                                                               c-CBL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-binding
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Best Local :
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Pfam: PF02761; Cbl_N2: 1.
Pfam: PF02762; Cbl_N3: 1.
Pfam: PF00627; UBA: 1.
Pfam: PF00097; zf-C3HC4: 1.
SMART; SM00185; UBA: 1.
SMART; SM00185; UBA: 1.
                                                                                                                                                             YM81_YEAST STANDARD; PRT; 1562 AA.
004781; Q04029;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 180.2 kDa protein in FAA4-HOR7 intergenic region.
YMR247C OR YM9408.09C OR YM9920.01C
                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
PIR; /
PDB; ]
                   Gentles S., Bowman S., Barrell B.G., Rajandream M.A., Walsh Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                SEQUENCE OF 950-1562 FROM N.A. STRAIN-S288C / AB972;
                                                                                            SEQUENCE OF 1-956 FROM N.A. STRAIN=S288C / AB972;
                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit inserved. Usage by and for commetric modified and this statement is not removed. Usage by and for commetric removed and this statement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                             Submitted
                                                                                     Hunt
                                                                                                                                    Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                               YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                Proto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00518; ZF_RING_1; 1. PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                         NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                        ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                          3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000449; InterPro; IPR001841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003153;
                                                                                                                                                                                                                                                                     380
                                                                                                                                                                                                                                                                                      3 LCTICSDFFDHSRDVAAIHCGHTFHLQCLIQWFETAPSRTCPQCRIQV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ween the Swiss Institute of Bioinformatics and the I
European Bioinformatics Institute. There are no resi
by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 UBA DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A43817;
1B47; 27
                                                                                     S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                    LCKICA---ENDKDVKIEPCGHLMCTSCLTSWQE-SEGQGCPFCRCEI 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X57110; CAA40393.1;
A43817; A43817.
                                                                                                                                                                                                                                                                                                                  Similarity
                                                                           Bowman S., Barrell
d (MAR-1995) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-99
                                                                                                                                                                                                                                                                                                                                                       906 AA;
                                                                                                                                                                                                                                                                                                                                                                 124
381
357
477
689
856
700
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear protein; Zinc-finger; Phosphorylation;
           STRONG,
                                                                                                                                                                                                                                                                                                                                                                         127
420
476
688
834
895
                                                                                                                                                                                                                                                                                                                  29.0%;
35.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UBA.
           To
                                                                                                                                                                                                                                                                                                                                                       MW;
           HUMAN
                                                                           B.G., Rajandream I
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                         8;
                                                                                                                                                                                                                                                                                                                  Score 85; DB 1;
Pred. No. 0.0041;
                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION.
7D686B050204AD8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   ASP/GLU-RICH (ACIDIC)
UBA.
                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR LOCALIZATION SIGNAL (POTENTIAL). RING-TYPE. ASP/GLU-RICH (ACIDIC). PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION.
           TYPE ZINC
V ZNF294.
                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                    Saccharomyces
                                                                                    M.A.,
                                                                                                                                                                                                                                                                                                         19;
                                                                            databases
                                                                                                                                                                                                                                                                                                                          Length 906
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                                                                                    Walsh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            restrictions on
                                                                                    S.V.;
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                                       S.V.;
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                            PROSITE; PS00518; ZF_RING_1; PROSITE; PS50089; ZF_RING_2;
          Hypothetical
ZN_FING
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Query Match
Best Local
                                                                                                                                                                  use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement /con him.
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01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 13.2 kDa protein in ORC2-TIP1 intergenic
YBR062C OR YBR0528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Zinc-finger ZN_FING 1508 1555 RING-SEQUENCE 1562 AA; 180185 MW C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGD; S0004861; YMR247C.
InterPro; IPRO1841; Znf_ring.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG
PROSITE; PS0089; ZF_RING_2; 1.
PROSITE; PS0089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                      Domdey H., Gassenhuber H., Obermaier B., Piravandi E.; Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
InterPro; IPR001841; Znf. pfam; PF00097; zf-C3HC4; SMART; SM00184; RING; 1.
                                                                    PIR; S45920; S45920.
SGD; S0000266; YBR062C
                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aljinovic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetales; NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                   EMBL;
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180185 MW; 97AC65E881362305 CRC64;
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                                                                                                                                 PROSITE; PS00405; 43_KD_POSTSYNAPTIC; PROSITE; PS00518; ZF_RING_1; FALSE_NEW PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                      PRINTS; PR00217; POSTSYNAPTIC.
PTODOM; PD012428; POSTSYNAPTIC;
SMART; SM000184; RING; 1.
SMART; SM00028; TPR; 5.
                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF000138; AAB63149.1;
InterPro; IPR001237; Postsyr
InterPro; IPR001440; TPR.
InterPro; IPR001841; Znf_rin
Pfam; PF00515; TPR; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no rest use by non-profit institutions as content modified and this statement is not removed. Usage by are entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
43 kDa receptor-associated protein of the synapse (RAPSYN)
(Acetylcholine receptor-associated 43 kDa protein) (43 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
Synapse; Postsynaptic membrane; Cytoskeleton; Myristate; Zinc-finger. Myristate; Zinc-finge 0 By SIMILARITY. 2N_FING 362 402 RING-TYPE.
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; Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata; Euteleostomi;
mes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .00068;
es 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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Best Local S
Matches 16
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SEQUENCE
                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hadano S., Ishida Y., Ikeda J.E.;
"The primary structure and genomic organization of five novel transcripts located close to the Huntington's disease gene on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Mammalia; Eutheria;
Transcription ZN_FING 1:
                                                                                                     EMBL; AB000468; BAA19122.1; -. EMBL; U95140; AAC52022.1; -.
                                                                                                                                                                                                                                          -1- TISSUE SPECIFICITY: WIDELY EXPRESSED AT TISSUES; HIGHLY EXPRESSED IN TESTIS.
-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FI
                                                                                                                                                                                                                                                                                                                                                              Genomics
                                                                                                                                                                                                                                                                                                                                                                                        Fusco A., Bruni C.B.;
"Identification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                Chiariotti L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome 4p16.3.";
DNA Res. 5:177-186(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98403881; PubMed=9734812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNF4_HUMAN
                      PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
                                                                InterPro; IPR001841; Znf,
Pfam; PF00097; zf-C3HC4;
                                                                                         MIM; 602850;
                                                                                                                                                                                                                                                                                                          SIMILARITY).
-!- SUBUNIT: INTERACTS WITH GSCL,
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98140125; PubMed=9479498;
                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                              (RNF4) mapping at 4p16.3.
Senomics 47:258-265(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                 similarity).
SUBCELLULAR LOCATION: Nuclear and cytoplasmic
                                                                                                                                                                                                                                                                                                                                    FUNCTION: ENHANCES ACTIVATION AS WELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGMCGESIGEKNNQLQALPCSHFFHLKCL----QTNGTRGCPNCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTICSDFF-DHSRDVAAIHCGHTFHLQCLIQWFETAPSRTCPQCR
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                                                     SM00184; RING;
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195
411 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 40, Created)
    regulation;
32 177
                                                                                                                                                                                                                                                                                                                                                                                                                Benvenuto G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND TISSUE SPECIFICITY
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35
                                                                         Znf_ring
                                                                                                                                                                                                                                                                                                                                     STEROID RECEPTOR-MEDIATED TRANSCRIPTIONAL AS ACTIVATING BASAL TRANSCRIPTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.8
              Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 84.5; D; Pred. No. 0.00 9; Mismatches
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PHOSPHORYLATION (POTENTIAL).
851E7B2F4645B459 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                Fedele M.,
    RING-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                             ANDROGEN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                        of
                                                                                                                                                                                                                                            ZINC FINGER.
              Zinc-finger;
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                Nuclear protein
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RRA ALL
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cuackenbush J.,
A Kadota K., Matsuda H.A., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Nasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
A Nasaki H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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16-OCT-2001 (Rel
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                                                          (RNF4) mapping at 4p16.3. Genomics 47:258-265(1998)
                                                                                                                                                                   MEDLINE=98140125; PubMed=9479498; Chiariotti L., Benvenuto G., Fedele
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Hayashizaki Y.;
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MEDLINE=21085660; PubMed=11217851;
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CD-1; TISSUE=Embryo;
MEDLINE=20284895; PubMed=10822263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                 Fusco
                                                                                                                                                                                                                                TISSUE=Embryo;
                                                                                                                                                                                                                                                          SEQUENCE OF 16-178 FROM N.A.
                                                                                                                                                                                                                                                                                                                     Submitted
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                                                                                                              "Identification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation
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                                  FUNCTION:
     ACTIVATION
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                                                                                                                                              A., Bruni C.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
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                                                                                                                                                                                                                                                                                                                  (FEB-2001)
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(Rel. 40,
(Rel. 40,
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     WELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Rodentia;
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     ^{\mathrm{AS}}
                                  STEROID
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     ACTIVATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
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                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                        full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
  RECEPTOR-MEDIATED TRANSCRIPTIONAL VATING BASAL TRANSCRIPTION (BY
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0.0013;
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Best Local
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16-0CT-2001
16-0CT-2001
16-0CT-2001
RING finger
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                                                                                                                                                                                              Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prosite; ps00518; zr_RING_1; 1.
prosite; ps50089; zr_RING_2; 1.
Transcription regulation; Activator; Zinc-finger; Nuclear protein.
                                                                                                                                                                                                                steroid
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNF4_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001841; Znf_ring. Pfam; PF00097; zf-C3HC4; 1. SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as modified and this statement is not re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 1 1
                                                                                                                                                                                                                                         "Identification of a novel RING finger
                                                                                                                                                                                                                                                             Palvimo J.J
                                                                                                                                                                                                                                                                               Moilanen A.-M., Poukka H.,
                                                                                                                                                                                                                                                                                                        MEDLINE=98378525; PubMed=9710597;
                                                                                                                                                                                                                                                                                                                               TISSUE=Testis
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1201691; Rnf4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
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                                                                                FUNCTION: ENHANCES STEROID RECEPTOR-MEDIATED TRANSCRIPTIONAL ACTIVATION AS WELL AS ACTIVATING BASAL TRANSCRIPTION.
SUBUNIT: INTERACTS WITH GSCL, ANDROGEN RECEPTOR AND TBP.
SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).

SUBUNIT: INTERACTS WITH GSCL, ANDROGEN RECEPTOR AND TBP.

SUBCELLULAR LOCATION: Nuclear and cytoplasmic.

SUBCELLULAR LOCATION: Nuclear and cytoplasmic.

TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED PRIMARILY IN THE DORAD.

EVELOPING NERVOUS SYSTEM WITH STRONG EXPRESSION IN THE ADOLLY.

ROOT GANCLIA AND GONADS. UBIQUITOUSLY EXPRESSED IN THE ADULT.

DEVELOPMENTAL STAGE: EXPRESSION IS DETECTED FROM EMBRYONIC DAND CONTINUES THROUGHOUT DEVELOPMENT AND INTO ADDLITHOOD.
                                          SIMILARITY: CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute.
                                                                 TESTIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPICMDGYSEIVQNGRLIVSTECGHVFCSQCLRDSLKNA--NTCPTCRKKI
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AK019171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U95141; AAC53539.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC003282;
                                                                                                                                                                        receptor mediated gene transcription."; ll. Biol. 18:5128-5139(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                               Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 40, (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 40, Created)
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in 4
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                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21910 MW;
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Last annotation update)
(SNURF).
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                                          1 RING-TYPE
                                                                                                                                                                                                                                                                                  Karvonen U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 84; DB Pred. No. 0.00 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                    0.A.,
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Best Local !
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01-DEC-1992
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HISSP: P20990, 1000.

InterPro; IPR001841; Znf_ring.

Pfam; PF0099; zf-C3HC4; 1.

SMART; SM00184; RING; 1.

PROSITE; PS00518; ZF_RING_1; 1.

PROSITE; PS50089; ZF_RING_2; 1.

PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 29
_HSVBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
Transcription regulation; Activator; Zinc-finger; Nuclear ZN_FING 136 181 RING-TYPE.
SEQUENCE 194 AA; 21896 MW; 40C13970FC11DFF2 CRC64;
                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=92219360; PubMed=1313901;
MITH U.V., Fraefel C., Vogt B., Vlcek C., Paces V., Schwyzer M.;
"Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1
- ", ~~rerminal and encode a putative zinc finger transactivator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovine herpesvirus type 1 (strain Jura)
Viruses; dsDNA viruses, no RNA stage; H
Alphaherpesvirinae; Varicellovirus.
NCBL_TaxID-31518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001841; Znf_ri
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF022081; AAC35248.1; -.
InterPro; IPR001841; Znf_ring.
                                                                                                                                                                         PIR; B38209; EDBE23.
HSSP; P28990; 1CHC.
                                                                                                                                                                                                                         EMBL; M84465; AAA46062.1; -
EMBL; AJ004801; CAA06138.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BICP0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .9/ER2.6).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CASEIN KINASE II.
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
SIMILARITY: TO OTHER HERPESVIRUSES ICPO PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71rol. 66:2763-2772(1992).
PTM: THE STRONGLY ACIDIC REGION MIGHT ACTIVATION DOMAIN, POSSIBLY REGULATED
                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 24, Created)
(Rel. 24, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Pred. No. 0.0013;
7; Mismatches 2
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                            2inc-finger;
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Best Local
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Best Local
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01-APR-1993
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                                                                                                                                                                                               DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Virol. 66:2763-2772(1992).
-I- PTM: THE STRONGLY ACIDIC REGION MIGHT ACTIVATION DOMAIN, POSSIBLY REGULATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92219360; PubMed=1313901; Wirth U.V., Fraefel C., Vogt B., Vlcek C., Paces V., Schwyzer M.; "Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus
                                                                                                                                                                                                                                       PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1
Transcription regulation; Trans-acting DNA-binding; Early protein; Repressor; ZN_FING 13 52 RING-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine herpesvirus type 1 (strain K22) Viruses; dsDNA viruses, no RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trans-acting 2.9/ER2.6).
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                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A38209; EDBE22.
HSSP; P28990; 1CHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-!- SIMILARITY: TO OTHER HERPESVIRUSES ICPO PROTEIN.
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10
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19; Conser
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676 /
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676
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(Rel. 25, Last sequence up)
(Rel. 40, Last annotation
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67701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Varicellovirus.
                                                                                                     28.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38
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••
                                                                                   Score 84; DB
Pred. No. 0.00
5; Mismatches
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                                                                                                                                                                                               ASP/GLU-RICH (ACIDIC).
; 9BB0683C9BFCA65D CRC64;
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No.
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                                                                                                                                                                                                                                                              factor; Activator; Phosphorylation.
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                                                                                   DB 1; Le 0.0042; hes 22;
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CREAR HUMAN

TID CHIEFHUMAN

TO CHARTYOLE MEREXORS (Chordata; Craniata; Vertebrata

TID CHIEFHUMAN

TID CHIEFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Nuclear (Potential).
ALTERNATIVE PRODUCTS: 3 ISOFORMS; A LONG FORM (SHOWN HERE)
TRUNCATED ISOFORM 1 AND TRUNCATED ISOFORM 2; ARE PRODUCED
ALTERNATIVE SPLICING.
      er; Phosphorylation; Alternative splicing.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
RING-TYPE.
PRO-RICH.
UBA.
MISSING (IN TRUNCATED ISOFORM 1).
DVFD -> TYRI (IN TRUNCATED ISOFORM 2).
MISSING (IN TRUNCATED ISOFORM 2).
MISSING (IN TRUNCATED ISOFORM 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G, KIDNEY, SPLEEN, AND TESTIS, HEMATOPOIETIC CELL LINES, BUS SALIVARY GLAND, OR SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FINGER
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RAPS_HUMAN

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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001237; F
InterPro; IPR001440; T
InterPro; IPR001841; Z
Pfam; PF00515; TPR; 5.
INIT_MET
ZN_FING
LIPID
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buckel A., Beeson D., James M., Vincent A.; "Cloning of cDNA encoding human rapsyn and mapping locus to chromosome 11p11.2-p11.1."; Genomics 35:613-616(1996).
                                                                                                                                                      PROSITE; PS00405; 43_KD_POSTSYNAPTIC; 1.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
PROSITE; PS50089; ZF_RING_2; 1.
Synapse; Postsynaptic membrane; Cytoskeleton;
                                                                                                                                                                                                                                                                 SMART; SM00184; RING; SMART; SM00028; TPR;
                                                                                                                                                                                                                                                                                                                   PRINTS; PR00217; POSTSYNAPTIC. ProDom; PD012428; Postsynaptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAPS_HUMAN Q13702;
                                                                                                                                Myristate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 601592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 233905; CAA83954.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97001170; PubMed=8812503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Muscl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
43 kDa receptor-associated protein of the synapse (RAPSYN)
(Acetylcholine receptor-associated 43 kDa protein) (43 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997

    -!- SIMILARITY: BELONGS TO THE RAPSYN FAMILY.
    -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   postsynaptic protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 LCKICA---ENDKDVKIEPCGHLMCTSCLTAWQE-SDGQGCPFCRCEI 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LCTICSDFFDHSRDVAAIHCGHTFHLQCLIQWFETAPSRTCPQCRIQV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON, POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN. SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: À CYSTEINE-RICH REGION HOMOLOGOUS TO PART OF THE REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE IMPORTANT II INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER. SIMILARITY: BELONGS TO THE RAPSYN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEMBRANES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an email to license@isb-sib.ch).
Zinc-finger.

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Primates;
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Pred. No. 0.00
8; Mismatches
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BY SIMILARITY.
RING-TYPE.
MYRISTATE (BY SIMILARITY).
PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
0.0059;
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                                                                                                                                                      Phosphorylation
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Best I
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                  SMART; SM00502; BBC; 1.
SMART; SM00336; BBOX; 1.
SMART; SM00336; BBOX; 1.
SMART; SM00449; RING; 1.
SMART; SM00449; SPRY; 1.
PROSITE; PSS0119; ZF_BBOX; 1.
PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A33_PLEWA
Q02084;
Q1-OCT-1994
                                                                                                                                                    Pfam; PF00622; SPRY; 1.
Pfam; PF00643; zf-B_box; 1.
Pfam; PF00097; zf-C3HC4; 1.
PRINTS; PR01406; BBOXZNFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                            InterPro; IPR001870; Gamma_carbxylse.
InterPro; IPR003877; SPRY.
InterPro; IPR003878; SPRY.domain.
InterPro; IPR000315; Znf_bbox.
InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bellini M., Lacroix J.-C., Gall J.G.;
"A putative zinc-binding protein on lampbrush chromosome loops.";
EMBO J. 12:107-114(1993).

-I- FUNCTION: MAY BE A NOCLEAR REGULATORY PROTEIN THAT IS STORED
IN THE GERMINAL VESICLE FOR USE DURING EARLY EMBRYOGENESIS
AND MAY PLAY A ROLE IN THE SYNTHESIS OR PROCESSING OF PRE-MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zinc-binding protein A33.

Pleurodeles waltlii (Iberian ribbed newt).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1994 (Rel.
01-OCT-1994 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003649; Bbox_C.
                                                                                                                                                                                                                                                                                                                                                    EMBL; L04190; AAA49614.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93154311; PubMed-7679068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-8319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pleurodeles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLUIAR LOCATION: Nuclear.

SUBCELLUIAR LOCATION: Nuclear.

BYMCLOPMENTAL STAGE: IT FIRST APPEARS ON THE CHROMOSOME LOOPS AND IN THE NUCLEOPLASM OF THE GERMINAL VESICLE (GV). IT IS TRANSMITTED TO THE EGG AT GV BREAKDOWN AND APPEARS IN EMBRYONIC NUCLEI AT THE MID-BLASTULA STAGE AND IS FOUND IN MANY BUT NOT ALL NUCLEI AT STILL LATER STAGES OF EMBRYOGENESIS.

SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

SIMILARITY: CONTAINS 1 B BOX-TYPE ZINC FINGER.

SIMILARITY: CONTAINS 1 SPRY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DURING OOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALCGESIGEKNSRLQALPCSHIFHLRCL----QNNGTRSCPNCR 402
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40,
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  protein; Developmental protein; Coiled
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annotation update)
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Pred. No. 0.00
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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InterPro; IPRO01841; Znf_ri;
Pf4m; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF_RING_1
PROSITE; PS50089; ZF_RING_2
                                                                                                                                                                                                                      EMBL; AJ010347; CAB40414.1; -. EMBL; AJ010346; CAB40413.1; -. EMBL; AL133621; CAB63747.1; -.
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                      Blum H., Bauersachs S., Mewes H.-W., Gassenhuber J., Wiemann Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-i- TISSUE SPECIFICITY: WEAKLY EXPRESSED IN PERIPHERAL BLOOD, PROSTATE, TESTIS AND OVARY.
-i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and characterization of RNF6, a mapping to 13q12."; Genomics 58:94-97(1999).
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MEDLINE=99265977; PubMed=10331950;
Macdonald D.H.C., Lahiri D., Sampa
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Pred. No. 0.0044;
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RING-TYPE.
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A Hattori M., Fujiyama A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
A Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
A Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
A Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
A Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
A Reichwald K., Rump A., Schillhabel N., Schudy A., Zimmermann W.,
A Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
A Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
A Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
A Minoshima S., Shinizu N., Mordsiek G., Hornischer K., Brandt P.,
A Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
A Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
A Mehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
A Lehrach H., Reinhardt R., Yaspo M.-L.;

"The DNA sequence of human chromosome 21.";

Nature 405:311-319(2000).
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                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                          EMBL; AL163249; CAB90430.1; -. EMBL; AL163248; CAB90429.3; -. EMBL; AB018257; BAA34434.1; -. Interpro; IPR001841; Znf_ring.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                     SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG
PROSITE; PS50089; ZF_RING_2; 1.
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SEQUENCE
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16-OCT-2001 (Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 18
                                                                                EMBL; X15788; CAA33789.1; -
EMBL; J03962; AAA40030.1; -
PIR; S04488; S04488
PIR; A31995; A31995.
MGD; MGI:99422; Rapsn.
                                  MGD; MGI:99422; Rapsn.
InterPro; IPR001237; Por
InterPro; IPR001440; TP
InterPro; IPR001841; Zn
Pfam; PF00515; TPR; 6.
                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1767
                                                                                                                                                                                                                                                       -!- DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO PART OF THE REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE IMPORTANT IN INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER.
-!- SIMILARITY: BELONGS TO THE RAPSYN FAMILY.
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1989 (Rel. 12, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
43 kDa receptor-associated protein of the synapse (RAPSYN)
(Acetylcholine receptor-associated 43 kDa protein) (43 kDa
          PRINTS; PR00217; POSTSYNAPTIC ProDom; PD012428; Postsynapti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Expression of RNA transcripts for the postsynaptic 43 kDa protein innervated and denervated rat skeletal muscle."; FEBS Lett. 249:229-233(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             postsynaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P12672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Froehner S.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89289985; PubMed=2737281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAPSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Rodentia;
                                               Znf_ring
                                                                        Postsynaptic
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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0.014;
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Best Local S
Matches 15
                    Query Match
Best Local
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-00V-1997 (Rel. 3
01-00V-1997 (Rel. 3
16-0CT-2001 (Rel. 4/
Hypothetical 64.7 kD
F26E4.11.
                                                                                                                                                                                                            InterPro; IPR003892; CUE.
InterPro; IPR001841; Znf_ring.
InterPro; IPR001841; Znf_ring.
Pfdam; PF002845; CUE; 1.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00546; CUE; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myristate;
INIT_MET
ZN_FING
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MOD_RES
CONFLICT
SEQUENCE
                                                                                                         Hypothetical I
ZN_FING 3:
SEQUENCE 56
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PROSITE; PS00405; 43_KD_POSTSYNAPTIC; 1.

PROSITE; PS00518; ZF_RING_1; FALSE_NEG.

PROSITE; PS50089; ZF_RING_2; 1.

Synapse; Postsynaptic membrane; Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BRISTOL N2;
Lightning J., Baynes C.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P90859; P90852;
01-NOV-1997 (Re
                                                                                                                                                                                                                                                                                                                                            EMBL; Z81070; CAB03009.1; --
EMBL; Z81075; CAB03009.1; JOINED
EMBL; Z81075; CAB03049.1; --
EMBL; Z81070; CAB03049.1; JOINED
WOrmPep; FZ6E4.11; CE09695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YUES_CAEEL
                                                                                                                                                                    PROSITE; PS00518; ZF_RING_1; FALSE_NEG PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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15; Conser
  l Similarity
16; Conserv
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362 402

1 1

195 195

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343 344
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  Conservative
                                                                                                           AA;
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40,
kDa
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                                                                                                           64709 MW;
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33.3%;
                 28.2%;
                                                                                                                                                    Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein F26E4.11 in chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                               JOINED.
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Pred. No. 0.00
10; Mismatches
  6,
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WRISTATE.

PHOSPHORYLATION (POTENTIAL).

PHOSPHORYLATION (POTENTIAL).

DV -> EL (IN REF. 2).
Score 82.5; DB 1;
Pred. No. 0.0054;
6; Mismatches 20;
                                                                                                         RING-TYPE.
; 7C790C238207E49B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1085A5C709FD1E56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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                                                                                                         CRC64;
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                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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5
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Gaps
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                                     MKR1_MOUSE
                                                                                       В
                                                  RESULT
                                                                                                                                    Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                         InterPro; IPR001395; Aldo_ket_re
InterPro; IPR001397; Zf-CCCH.
InterPro; IPR001841; Znf_ring.
Pfam; PF00097; Zf-C3HC4; 1.
Pfam; PF00642; Zf-CCCH; 4.
SMART; SM00184; RING; 1.
SMART; SM00186; ZF_RING_1; 1.
PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS00518; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9TT91;
01-MAR-2002
01-MAR-2002
01-MAR-2002
                                                                                                                                                                                              ZN_FING
ZN_FING
SEQUENCE
                                                                                                                                                                                                                                   ZN_FING
ZN_FING
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MACEU
MKR1_MOUSE STANDARD;
O9QXP6;
O1-MAR-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gray T.A., Hernandez L., Carey A.H., Schaldach M.A., Smithwick N
Rus K., Marshall Graves J.A., Stewart C.L., Nicholls R.D.;
"The ancient source of a distinct gene family encoding proteins
featuring RING and C(3)H zinc-finger motifs with abundant expres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in developing brain and nervous system."; Genomics 66:76-86(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-20304755; PubMed-10843807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Metatheria; Diprotodontia;
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF192786; AAF17489.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macropus eugenii (Tammar wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKRN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Makorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKR1_MACEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                  linc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 CVVCWELLGTSR----RLPCSHQFHDWCLMWWL---AQDSSCPTCRCTI
                                                                                       276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                            3 LCTICSDFF-----
                                                                                       VCGICMEVVYEKANPSERRFGILSNCNHTYCLKCIRKWRSAKQFESKIIKSCPECRI
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232
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; Pred. No. 0.00
11; Mismatches
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C3H1-TYPE 2.
C3H1-TYPE 3.
MAKORIN-TYPE.
RING-TYPE.
C3H1-TYPE 4.
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CB2D9B147433853E CRC64
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(See http://www.isb-sib.
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RESULT 40

MKR1_HUMAN

ID MKR1_HUMAN

AC Q9UHC7; Q9UE2

DT 01-MAR-2002 (
C 01 MAR-2002 (
C 02 MARN1 (
C 03 Homo sapiens

OC Eukaryota; Me

OC Mammalia; Eut

OX NCBI_TaxID=96

RN [1]

RP SEQUENCE FROM

MEDLINE=20304
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                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
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Pfam: PF000642; zf-C3CCH; 4.
SMART; SM00184; RING; 1.
SMART; SM00356; ZnF_C3H1; 4.
PROSITE; PS00518; ZF_RING_1; 1
PROSITE; PS00518; ZF_RING_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; C
Mammalia; Eutheria; F
NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The ancient source of a distinct gene family encoding profesting RING and C(3)H zinc-finger motifs with abundant in developing brain and nervous system.";

Genomics 66:76-86(2000).
    SEQUENCE FROM N.A. MEDLINE=20304755;
                                                Homo sapiens (Human Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                         ZN_FING
ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           ZN_FING
ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1859353; Mkrn1
InterPro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
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                                        NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                             ZN_FING
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InterPro; IPR001841; Znf_ring.
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01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 RING-TYPE ZINC SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC
                                                                                                                                                                                                                VCGICMEVVYEKANPSERRFGILSNCNHTYCLKCIRKWRSAKQFESKIIKSCPECRI
                                                                                                                                                                                                                                         LCTICSDFF-----DHSRDVAAIHCGHTFHLQCLIQW-----FETAPSRTCPQCRI
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Metazoa; Chordata; C
Metazoa; Rodentia;
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Last annotation update)
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C3H1-TYPE 2.
C3H1-TYPE 3.
C3H1-TYPE 3.
MAKORIN-TYPE CYS-HIS.
RING-TYPE.
C3H1-TYPE 4.
C3H1-TYPE 4.
C6H1-TYPE 4.
                                                                                                                                                                                                                                                            Score 81.5; DB 1
Pred. No. 0.0062;
1; Mismatches 1
                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                          PRT;
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Sciurognathi; Muridae;
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EMBL; AF192792; AAF18979.1; JOINI
EMBL; AL136812; CAB66746.1; ...
InterPro; IPRO00571; Zf-CCCH.
InterPro; IPRO10841; Znf_ring.
Pfam; PF00097; Zf-G3HC4; 1.
Pfam; PF00642; Zf-CCCH; 4.
                                                                                                      CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mewes H.-W., Ottenwaelder B., Obermaier B., Wambutt R., Korn B., Klein M., Poustka A., "Towards a catalog of human genes and protei analysis of 500 novel complete protein codin Genome Res. 11:422-435(2001).
                                                                                                                                                  ZN_FING
                                                                                                                                                                                                                               SMART; SM00184; RING; 1.
SMART; SM00356; ZnF_CA1; 4.
PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
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                                                                                                                                                                                                ZN_FING
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-!- SIMILARITY: CONTAINS 4 C3H1-TYPE
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                                                                                                                                        VARIANT
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VCGICMEVVYEKANPSERRFGILSNCNHTYCLKCIRKWRSAKQFESKIIKSCPECRI
                      LCTICSDFF-----DHSRDVAAIHCGHTFHLQCLIQW-----FETAPSRTCPQCRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n S., Weil B., Wellenreuther R., Gassenhuber J., Glassle W., Boecher M., Bloecker H., Bauersachs S., Blum H., J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner
                                              . Similarity
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JOINED.
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C3H1-TYPE 2.
C3H1-TYPE 3.
MAKORIN-TYPE CYS-HIS.
RING-TYPE.
C3H1-TYPE 4.
L -> V
FTId=VAR_012161.
GR -> AG (IN REF. 1; A
                                             Score 81.5; D
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n coding human cDNAs.
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